A study of the TAS2R38 gene was also conducted through use of bioinformatics. The BLAST program available at www.ncbi.nlm.nih.gov was used to compare the PTC tasting forward primer to other similar DNA sequences. The predicted length of the amplicon (the product sequence from PCR) was then determined through analysis of the forward and reverse primer sequences and the chromosome location of the TAS2R38 was found using the Map Viewer Option which provides an ideogram of the chromosome in its entirety. The PTC taster sequence and the PTC non-taster sequence were compared to other similar TAS2R38 genes from chimpanzees, bonobos, and gorillas using the Bioservers Internet site at the Dolan DNA Leaner Center. This is found at www.bioservers.org. Through this program, the sequences for the human PTC taster gene was compared to the human PTC non-taster gene and the TAS2R38 amplicon; the sequence for the human PTC taster gene was compared to the human PTC non-taster gene, the chimpanzee sequence, the bonobo sequence, and the gorilla sequence; and the sequence for the forward primer of the human PTC tasting gene was compared to the human PTC tasting gene and the human PTC non-tasting gene. Comparisons of these DNA sequences revealed critical SNPs which resulted in a change to an amino acid and the protein sequence overall. After comparing these sequences, the lengths of the non-taster PCR product and the taster PCR product were determined based upon the mechanism of the restriction enzyme HaeII. This aided in the analysis of the bands on the DNA gel ("Part 2: Bioinformatics of the TAS2R38 gene" 5-9).

Results:

lead in Tell a story about your experiment
Better

The location of the bands on the DNA gel led to the determination of my genotype for the PTC tasting gene. Based upon the experimental evidence from the tasting stick which indicated my phenotype to be a moderate taster, my genotype should have been either homozygous dominant or heterozygous ~~dominant~~ based upon the number of base pairs in the digested DNA fragment. The bands on the DNA gel should have been at about 176 nucleotides and 43 nucleotides to correlate with the phenotype I recorded from the tasting stick experiment. The results for both my undigested and digested PCR product were inconclusive due to experimental error: there were no bands formed on the agarose gel (see Figure 1). This experimental error could have occurred due to a perforation of the DNA gel during the loading of both PCR products. The pipette most likely poked a hole in the bottom of one or both lanes, causing both samples to leak out and render the gel electrophoresis with no result. A lack of bands in the DNA gel could also have resulted from an error in following the experimental protocol. I would have expected to have seen bands at the appropriate locations for either a homozygous/heterozygous taster based upon my phenotype. I either possess two dominant alleles or one dominant and one recessive allele. The members of my group all possessed taster phenotypes. Two of their results were conclusive; the experiment proved that their genotype matched their phenotype. The third member of my group also experienced experimental error in her lanes of the gel, probably for the same missteps.

Good
ok
↳ DNA collected/amplif

My class overall had a ratio of 7 tasters to 4 non-tasters based upon the gel results. This is a percentage of about 64% to 36% which is approximately the ratio of tasters to non-tasters in a given population. Therefore, the results from our lab group as a whole are concurrent with the genomic ratios normally occurring within society. The ratio for all genetics lab was about 46 tasters to 18 non-tasters. This is a percentage of approximately 72% to 28% which is also nearly concurrent with the genomic ratios normally occurring within a population (see Table 1). There were inconsistencies in the data collected from my class. Two individuals recorded a phenotype of taster that did not correspond to the genotype obtained through use of a DNA gel. This could be due to an error in the preparation of cheek cells or amplified DNA for PCR or an error adding the restriction enzyme. An error most likely did not occur during PCR because the majority of the class received consistent results or during the loading of

Good